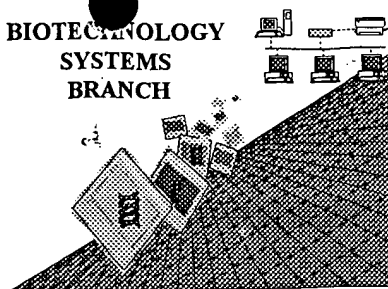


RAW SEQUENCE LISTING **ERROR REPORT**

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/720,363

Source: P469

Date Processed by STIC: 2/17/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

BEST AVAILABLE COPY

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/220,363

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000

- 9 Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ✓ Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

PCT09

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/720,363

DATE: 07/17/2001

TIME: 11:18:08

Input Set : A:\Sequen-1.doc

Output Set: N:\CRF3\07172001\I720363.raw

Does Not Comply
Corrected Diskette Needed

1 <110> APPLICANT: Arima, Hidetoshi
 3 Tsuchiya, Seishi
 5 Hirata, Takahiro
 7 Akiyama, Katsuhiko
 9 Goto, Takashi
 11 <120> TITLE OF INVENTION: Antisense Oligonucleotide Inhibiting IL-10 Protein
 13 Expression
 14 0 <130> FILE REFERENCE:
 15 <140> CURRENT APPLICATION NUMBER: US/09/720,363
 17 <141> CURRENT FILING DATE: 2001-06-04
 19 <150> PRIOR APPLICATION NUMBER: PCT/JP99/03315
 W--> 21 <151> PRIOR FILING DATE: 1999-22-06 1999-06-22 ← use this date format
 23 <160> NUMBER OF SEQ ID NOS: 9

ERRORED SEQUENCES

28 <210> SEQ ID NO: 1
 30 <211> LENGTH: 18
 32 <212> TYPE: DNA
 C--> 34 <213> ORGANISM: Nucleic Acid Artificial DNA
 W--> 36 <220> FEATURE: Feature of sequence: Corresponding to from +176 to +193 of
 W--> 38 SEQ ID NO: 9
 40 <223> OTHER INFORMATION: Antisense: YES, Single Strand, Topology: Straight
 42 <400> SEQUENCE: 1
 E--> 44 agaaggtctt cactctgc use lower-case letters for all bases 18 ← insert cumulative base total at right margin of each line
 46 <210> SEQ ID NO: 2
 48 <211> LENGTH: 18
 50 <212> TYPE: DNA
 C--> 52 <213> ORGANISM: Nucleic Acid Artificial DNA
 W--> 54 <220> FEATURE: Feature of sequence: Corresponding to from +181 to +198 of
 W--> 55 SEQ ID NO: 9
 57 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
 59 <400> SEQUENCE: 2
 E--> 61 ttgaaagaaa gtcttcac 18 ←
 64 <210> SEQ ID NO: 3
 66 <211> LENGTH: 18
 68 <212> TYPE: DNA
 C--> 70 <213> ORGANISM: Nucleic Acid Artificial DNA
 W--> 72 <220> FEATURE: Feature of sequence: Corresponding to from +367 to +384 of
 W--> 74 SEQ ID NO: 9
 76 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
 78 <400> SEQUENCE: 3
 E--> 80 ggtcttcagg ttctcccc ← insert total
 83 <210> SEQ ID NO: 4
 85 <211> LENGTH: 18
 87 <212> TYPE: DNA

see item 10 on Error Summary Sheet
*This goes on 2237 line**
delete - not needed in new sequence
Rules format
** DO NOT insert any response to 2207; 2207 is a "header" only.*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/720,363

DATE: 07/17/2001
TIME: 11:18:08

Input Set : A:\Sequen-1.doc
Output Set: N:\CRF3\07172001\I720363.raw

same error

C--> 89 <213> ORGANISM: Nucleic Acid Artificial DNA
W--> 91 <220> FEATURE: Feature of sequence: Corresponding to from +637 to +654 of
W--> 93 SEQ ID NO:9
95 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
97 <400> SEQUENCE: 4
E--> 99 ctgggtcagc tatccca_g
102 <210> SEQ ID NO: 5
104 <211> LENGTH: 18
106 <212> TYPE: DNA
same
C--> 108 <213> ORGANISM: Nucleic Acid Artificial DNA
W--> 110 <220> FEATURE: Feature of sequence: Corresponding to from +915 to +932 of
W--> 112 SEQ ID NO:9
114 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
116 <400> SEQUENCE: 5
E--> 118 gcttggaatg gaagcttc
121 <210> SEQ ID NO: 6
123 <211> LENGTH: 18
125 <212> TYPE: DNA
127 <213> ORGANISM: Nucleic Acid Synthesized DNA
same
W--> 129 <220> FEATURE: Feature of Sequence: Corresponding to from +1246 to +1263
W--> 131 of SEQ ID NO:9
133 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
135 <400> SEQUENCE: 6
E--> 137 ggctggtag gaa_gctcct
140 <210> SEQ ID NO: 7
142 <211> LENGTH: 18
144 <212> TYPE: DNA
same
C--> 146 <213> ORGANISM: Nucleic Acid Artificial DNA
W--> 148 <220> FEATURE: Feature of sequence: Corresponding to from +1249 to +1266 of
W--> 150 SEQ ID NO:9
152 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
154 <400> SEQUENCE: 7
E--> 156 ccaggtggt taggaact
159 <210> SEQ ID NO: 8
161 <211> LENGTH: 18
163 <212> TYPE: DNA
same
C--> 165 <213> ORGANISM: Nucleic Acid Artificial DNA
W--> 167 <220> FEATURE: Feature of sequence: Mouse IL-10 protein gene
169 <223> OTHER INFORMATION: Single-strand, Topology: Straight, Antisense: YES
171 <400> SEQUENCE: 8
E--> 173 aggtcctgga gtccagca

See next page for more errors

<213> CDNA *see item 10 on Enr Summary Sheet*

<220> ~~Feature of sequence:~~ CDNA of Human IL-10 protein
delete

<223> ~~Single-strand, Topology: Straight, Antisense: No~~
delete

move to <223> line

<400> 9

AAACCACAAG ACAGACTTGC AAAAGAAGGC ATGCACAGCT 40
CAGCACTGCT CTGTTGCCTG GTCCTCCTGA CTGGGGTGAG 80
GGCCAGCCCA GGCCAGGGCA CCCAGTCTGA GAACAGCTGC 120
ACCCACTTCC CAGGCAACCT GCCTAACATG CTTGAGATC 160
TCCGAGATGC CTTGAGCAGA GTGAAGACTT TCTTTCAAAT 200
GAAGGATCAG CTGGACAACT TGTGTGTTAA GGAGTCCTTG 240
CTGGAGGACT TTAAGGGTTA CCTGGGTTGC CAAGCCTTGT 280
CTGAGATGAT CCAGTTTTAC CTGGAGGAGG TGATGCCCCA 320
AGCTGAGAAC CAAGACCCAG ACATCAAGGC GCATGTGAAC 360
TCCCTGGGGG AGAACCTGAA GACCCTCAGG CTGAGGCTAC 400
GGCGCTGTCA TCGATTTCTT CCCTGTGAAA ACAAGAGCAA 440
GGCCGTGGAG CAGGTGAAGA ATGCCTTTAA TAAGCTCCAA 480
GAGAAAGGCA TCTACAAAGC CATGAGTGAG TTTGACATCT 520
TCATCAACTA CATAGAAGCC TACATGACAA TGAAGATACG 560
AAACTGAGAC ATCAGGGTGG CGACTCTATA GACTCTAGGA 600
CATAAATTAG AGGTCTCCAA AATCGGATCT GGGGCTCTGG 640
GATAGCTGAC CCAGCCCCTT GAGAAACCTT ATTGTACCTC 680
TCTTATAGAA TATTTATTAC CTCTGATACC TCAACCCCCA 720
TTTCTATTTA TTTACTGAGC TTCTCTGTGA ACGATTTAGA 760
AAGAAGCCCA ATATTATAAT TTTTTTCAAT ATTTATTATT 800
TTCACCTGTT TTTAAGCTGT TTCCATAGGG TGACACACTA 840
TGGTATTTGA GTGTTTTAAG ATAAATTATA AGTTACATAA 880
GGGAGGAAAA AAAATGTTCT TTGGGGAGCC AACAGAAGCT 920
TCCATTCCAA GCCTGACCAC GCTTTCTAGC TGTTGAGCTG 960
TTTTCCCTGA CCTCCCTCTA ATTTATCTTG TCTCTGGGCT 1000
TGGGGCTTCC TAACTGCTAC AAATACTCTT AGGAAGAGAA 1040

use lower-case letters for bases (portion of seq 9)

All sample Sequence Listings (attached) for valid format

<110> Smith, John; Smithgene Inc.

<120> Example of a Sequence Listing

<130> 01-00001

<140> PCT/EP98/00001

<141> 1998-12-31

<150> US 08/999,999

<151> 1997-10-15

<160> 4

<170> PatentIn version 2.0

<210> 1

<211> 389

<212> DNA

<213> Paramecium sp.

<220>

<221> CDS

<222> (279)...(389)

<300>

<301> Doe, Richard

<302> Isolation and Characterization of a Gene Encoding a
Protease from Paramecium sp.

<303> Journal of Genes

<304> 1

<305> 4

<306> 1-7

<307> 1988-06-31

<308> 123456

<309> 1988-06-31

<400> 1

agctgtagtc	attcctgtgt	cctcttctct	ctgggcttct	caccctgcta	atcagatctc	60
agggagagtg	tcttgaccct	cctctgcctt	tgcagcttca	caggcaggca	ggcaggcagc	120
tgatgtggca	attgctggca	gtgccacagg	cttttcagcc	aggcttaggg	tgggttcgcg	180
cgcggcgcg	cggccctct	cgcgctcctc	tcgcgcctct	ctctcgctct	cctctcgctc	240

Appendix 3, page 2

ggacctgatt	aggtgagcag	gaggaggggg	cagtttagc	atg Met 1	gtt Val	tca Ser	atg Met	ttc Phe 5	agc Ser	296						
ttg Leu	tct Ser	ttc Phe	aaa Lys 10	tgg Trp	cct Pro	gga Gly	ttt Phe	tgt Cys 15	ttg Leu	ttt Phe	gtt Val	tgt Cys	ttg Leu 20	ttc Phe	caa Gln	344
tgt Cys	ccc Pro	aaa Lys 25	gtc Val	ctc Leu	ccc Pro	tgt Cys	cac His 30	tca Ser	tca Ser	ctg Leu	cag Gln	ccg Pro 35	aat Asn	ctt Leu	389	

<210> 2
<211> 37
<212> PRT
<213> Paramecium sp.

<400> 2	Met 1	Val	Ser	Met	Phe 5	Ser	Leu	Ser	Phe	Lys 10	Trp	Pro	Gly	Phe	Cys 15	Leu
	Phe	Val	Cys	Leu 20	Phe	Gln	Cys	Pro	Lys 25	Val	Leu	Pro	Cys	His 30	Ser	Ser
	Leu	Gln	Pro 35	Asn	Leu											

<210> 3
<211> 11
<212> PRT
<213> Artificial Sequence

<220>
<223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3	Met 1	Val	Asn	Leu	Glu 5	Pro	Met	His	Thr	Glu 10	Ile
---------	----------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----

<210> 4
<400> 4
000

[Annex VIII follows]

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M, when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO: #:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example; US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/720,363

DATE: 07/17/2001
TIME: 11:18:09

Input Set : A:\Sequen~1.doc
Output Set: N:\CRF3\07172001\I720363.raw

L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:15 M:270 C: Current Application Number differs, Replaced Current Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:21 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:34 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:1
L:36 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:38 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:44 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:1
L:44 M:112 C: (48) String data converted to lower case,
L:52 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:2
L:54 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:55 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:61 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:2
M:112 Repeated in SeqNo=2
L:70 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:3
L:72 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:74 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:80 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:3
M:112 Repeated in SeqNo=3
L:89 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:4
L:91 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:93 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:99 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:4
M:112 Repeated in SeqNo=4
L:108 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:5
L:110 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:112 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:118 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:5
M:112 Repeated in SeqNo=5
L:129 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:131 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:137 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:6
M:112 Repeated in SeqNo=6
L:146 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:7
L:148 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:150 M:259 W: Allowed number of lines exceeded, <220> FEATURE:
L:156 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:7
M:112 Repeated in SeqNo=7
L:165 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:8
L:167 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:173 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:18 SEQ:8
M:112 Repeated in SeqNo=8
L:184 M:256 W: Invalid Numeric Header Field, <220> has non-blank data
L:190 M:112 C: (48) String data converted to lower case,
M:112 Repeated in SeqNo=9

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